

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/530,457
Source: IFWP
Date Processed by STIC: 7/5/06

ENTERED



IFWP

RAW SEQUENCE LISTING DATE: 07/05/2006
 PATENT APPLICATION: US/10/530,457 TIME: 14:11:17

Input Set : A:\1-32709A FMI SEQ LIST.txt
 Output Set: N:\CRF4\07052006\J530457.raw

```

4 <110> APPLICANT: HOFSTEENGE; Jan
5     KEUSCH; Jeremy
7 <120> TITLE OF INVENTION: ASSAYS FOR C-MANNOSYLTRANSFERASE
10 <130> FILE REFERENCE: 1-32709A/FMI
12 <140> CURRENT APPLICATION NUMBER: 10/530,457
C--> 13 <141> CURRENT FILING DATE: 2005-04-05
15 <150> PRIOR APPLICATION NUMBER: PCT/EP03/011139
16 <151> PRIOR FILING DATE: 2003-10-08
18 <150> PRIOR APPLICATION NUMBER: GB0223449
19 <151> PRIOR FILING DATE: 2002-10-09
21 <160> NUMBER OF SEQ ID NOS: 9
23 <170> SOFTWARE: FastSEQ for Windows Version 4.0
25 <210> SEQ ID NO: 1
26 <211> LENGTH: 6
27 <212> TYPE: PRT
28 <213> ORGANISM: Artificial Sequence
30 <220> FEATURE:
31 <221> NAME/KEY: PEPTIDE
32 <222> LOCATION: (1)...(6)
33 <223> OTHER INFORMATION: C-mannosyltransferase (CMT) substrate
35 <223> OTHER INFORMATION: Synthetic peptide
W--> 37 <400> 1
38 Ala Trp Ala Lys Trp Ala
39 1           5
42 <210> SEQ ID NO: 2
43 <211> LENGTH: 111
44 <212> TYPE: DNA
45 <213> ORGANISM: Artificial Sequence
47 <220> FEATURE:
48 <221> NAME/KEY: protein_bind
49 <222> LOCATION: (1)...(111)
50 <223> OTHER INFORMATION: A forward primer carrying the signal sequence from
51     eosinophil derived neurotoxin
53 <221> NAME/KEY: misc_feature
54 <222> LOCATION: (19)...(79)
55 <223> OTHER INFORMATION: Signal sequence from eosinophil derived neurotoxin
56     (EON
58 <223> OTHER INFORMATION: Synthetic oligonucleotide
W--> 60 <400> 2
61 acagaagctt ccaccaatgg ttccaaaact gacttcccaa atttgtcttc ttctgttggg 60
62 gcttctggct gtggagggt cactccatgt ctcccctata ctaggttatt g          111
64 <210> SEQ ID NO: 3
65 <211> LENGTH: 55

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66 <212> TYPE: DNA
67 <213> ORGANISM: Artificial Sequence
69 <220> FEATURE:
70 <221> NAME/KEY: primer_bind
71 <222> LOCATION: (1)...(55)
72 <223> OTHER INFORMATION: A reverse primer encoding the CMT substrate site
74 <223> OTHER INFORMATION: Synthetic oligonucleotide
W--> 76 <400> 3
77 atatgaattc tcagtcagtc aagcccatTT agcccaagcg gatccacgcg gaacc      55
79 <210> SEQ ID NO: 4
80 <211> LENGTH: 50
81 <212> TYPE: DNA
82 <213> ORGANISM: Artificial Sequence
84 <220> FEATURE:
85 <221> NAME/KEY: primer_bind
86 <222> LOCATION: (1)...(50)
87 <223> OTHER INFORMATION: Forward primer
89 <221> NAME/KEY: misc_feature
90 <222> LOCATION: (14)...(19)
91 <223> OTHER INFORMATION: Hind III restriction site
W--> 93 <221> misc_feature
94 <222> LOCATION: (20)...(30)
95 <223> OTHER INFORMATION: Kozak sequence
97 <223> OTHER INFORMATION: Synthetic oligonucleotide
W--> 99 <400> 4
100 ggggtaccag atctaagctt gccaccatgg ccaagggctt ctatatttcc      50
102 <210> SEQ ID NO: 5
103 <211> LENGTH: 50
104 <212> TYPE: DNA
105 <213> ORGANISM: Artificial Sequence
107 <220> FEATURE:
108 <221> NAME/KEY: protein_bind
109 <222> LOCATION: (1)...(50)
110 <223> OTHER INFORMATION: Reverse primer
112 <221> NAME/KEY: misc_feature
113 <222> LOCATION: (2)...(7)
114 <223> OTHER INFORMATION: Spe I sequence
W--> 116 <221> misc_feature
117 <222> LOCATION: (8)...(29)
118 <223> OTHER INFORMATION: A tobacco etch virus (TEV) protease site
120 <223> OTHER INFORMATION: Synthetic oligonucleotide
W--> 122 <400> 5
123 gactagtacc ctgaaaatac aaattctcac tttggtccaa ggtggtggcc      50
125 <210> SEQ ID NO: 6
126 <211> LENGTH: 28
127 <212> TYPE: DNA
128 <213> ORGANISM: Artificial Sequence
130 <220> FEATURE:
131 <221> NAME/KEY: primer_bind

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132 <222> LOCATION: (1)...(28)
133 <223> OTHER INFORMATION: Forward primer
135 <221> NAME/KEY: misc_feature
136 <222> LOCATION: (2)...(7)
137 <223> OTHER INFORMATION: Spe I restriction site
139 <223> OTHER INFORMATION: Synthetic oligonucleotide
W--> 141 <400> 6
142 gactagttcc cctatactag gttattgg 28
144 <210> SEQ ID NO: 7
145 <211> LENGTH: 42
146 <212> TYPE: DNA
147 <213> ORGANISM: Artificial Sequence
149 <220> FEATURE:
150 <221> NAME/KEY: primer_bind
151 <222> LOCATION: (1)...(42)
152 <223> OTHER INFORMATION: Reverse primer
154 <221> NAME/KEY: misc_feature
155 <222> LOCATION: (9)...(14)
156 <223> OTHER INFORMATION: Spe I restriction site
158 <223> OTHER INFORMATION: Synthetic nucleotide
W--> 160 <400> 7
161 gctctagaga attcctatca agccactga gcccaagcgg at 42
163 <210> SEQ ID NO: 8
164 <211> LENGTH: 924
165 <212> TYPE: DNA
166 <213> ORGANISM: Artificial Sequence
168 <220> FEATURE:
169 <221> NAME/KEY: CDS
170 <222> LOCATION: (1)...(924)
171 <223> OTHER INFORMATION: The cDNA sequence of the pSMCi-APN-GST-AWAQWA
172 insert
174 <223> OTHER INFORMATION: Engineered sequence
W--> 176 <400> 8
177 atg gcc aag ggc ttc tat att tcc aag tcc ctg ggc atc ctg ggg atc 48
178 Met Ala Lys Gly Phe Tyr Ile Ser Lys Ser Leu Gly Ile Leu Gly Ile
179 1 5 10 15
181 ctc ctg ggc gtg gca gcc gtg tgc aca atc atc gca ctg tca gtg gtg 96
182 Leu Leu Gly Val Ala Ala Val Cys Thr Ile Ile Ala Leu Ser Val Val
183 20 25 30
185 tac tcc cag gag aag aac aag aac gcc aac agc tcc ccc gtg gcc tcc 144
186 Tyr Ser Gln Glu Lys Asn Lys Asn Ala Asn Ser Ser Pro Val Ala Ser
187 35 40 45
189 acc acc ccg tcc gcc tca gcc acc acc aac ccc gcc tcg gcc acc acc 192
190 Thr Thr Pro Ser Ala Ser Ala Thr Thr Asn Pro Ala Ser Ala Thr Thr
191 50 55 60
193 ttg gac caa agt gag aat ttg tat ttt cag ggt act agt tcc cct ata 240
194 Leu Asp Gln Ser Glu Asn Leu Tyr Phe Gln Gly Thr Ser Ser Pro Ile
195 65 70 75 80
197 cta ggt tat tgg aaa att aag ggc ctt gtg caa ccc act cga ctt ctt 288

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```

198 Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro Thr Arg Leu Leu
199      85      90      95
201 ttg gaa tat ctt gaa gaa aaa tat gaa gag cat ttg tat gag cgc gat 336
202 Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu Tyr Glu Arg Asp
203      100      105      110
205 gaa ggt gat aaa tgg cga aac aaa aag ttt gaa ttg ggt ttg gag ttt 384
206 Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu Gly Leu Glu Phe
207      115      120      125
209 ccc aat ctt cct tat tat att gat ggt gat gtt aaa tta aca cag tct 432
210 Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys Leu Thr Gln Ser
211      130      135      140
213 atg gcc atc ata cgt tat ata gct gac aag cac aac atg ttg ggt ggt 480
214 Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn Met Leu Gly Gly
215 145      150      155      160
217 tgt cca aaa gag cgt gca gag att tca atg ctt gaa gga gcg gtt ttg 528
218 Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu Gly Ala Val Leu
219      165      170      175
221 gat att aga tac ggt gtt tcg aga att gca tat agt aaa gac ttt gaa 576
222 Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser Lys Asp Phe Glu
223      180      185      190
225 act ctc aaa gtt gat ttt ctt agc aag cta cct gaa atg ctg aaa atg 624
226 Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu Met Leu Lys Met
227      195      200      205
229 ttc gaa gat cgt tta tgt cat aaa aca tat tta aat ggt gat cat gta 672
230 Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn Gly Asp His Val
231      210      215      220
233 acc cat cct gac ttc atg ttg tat gac gct ctt gat gtt gtt tta tac 720
234 Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp Val Val Leu Tyr
235 225      230      235      240
237 atg gac cca atg tgc ctg gat gcg ttc cca aaa tta gtt tgt ttt aaa 768
238 Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu Val Cys Phe Lys
239      245      250      255
241 aaa cgt att gaa gct atc cca caa att gat aag tac ttg aaa tcc agc 816
242 Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr Leu Lys Ser Ser
243      260      265      270
245 aag tat ata gca tgg cct ttg cag ggc tgg caa gcc acg ttt ggt ggt 864
246 Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala Thr Phe Gly Gly
247      275      280      285
249 ggc gac cat cct cca aaa tcg gat ctg gtt ccg cgt gga tcc gct tgg 912
250 Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg Gly Ser Ala Trp
251      290      295      300
253 gct cag tgg gct 924
254 Ala Gln Trp Ala
255 305
258 <210> SEQ ID NO: 9
259 <211> LENGTH: 308
260 <212> TYPE: PRT
261 <213> ORGANISM: Artificial Sequence
263 <220> FEATURE:

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264 <223> OTHER INFORMATION: Engineered sequence

266 <400> SEQUENCE: 9

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267 Met Ala Lys Gly Phe Tyr Ile Ser Lys Ser Leu Gly Ile Leu Gly Ile
268 1 5 10 15
269 Leu Leu Gly Val Ala Ala Val Cys Thr Ile Ile Ala Leu Ser Val Val
270 20 25 30
271 Tyr Ser Gln Glu Lys Asn Lys Asn Ala Asn Ser Ser Pro Val Ala Ser
272 35 40 45
273 Thr Thr Pro Ser Ala Ser Ala Thr Thr Asn Pro Ala Ser Ala Thr Thr
274 50 55 60
275 Leu Asp Gln Ser Glu Asn Leu Tyr Phe Gln Gly Thr Ser Ser Pro Ile
276 65 70 75 80
277 Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro Thr Arg Leu Leu
278 85 90 95
279 Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu Tyr Glu Arg Asp
280 100 105 110
281 Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu Gly Leu Glu Phe
282 115 120 125
283 Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys Leu Thr Gln Ser
284 130 135 140
285 Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn Met Leu Gly Gly
286 145 150 155 160
287 Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu Gly Ala Val Leu
288 165 170 175
289 Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser Lys Asp Phe Glu
290 180 185 190
291 Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu Met Leu Lys Met
292 195 200 205
293 Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn Gly Asp His Val
294 210 215 220
295 Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp Val Val Leu Tyr
296 225 230 235 240
297 Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu Val Cys Phe Lys
298 245 250 255
299 Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr Leu Lys Ser Ser
300 260 265 270
301 Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala Thr Phe Gly Gly
302 275 280 285
303 Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg Gly Ser Ala Trp
304 290 295 300
305 Ala Gln Trp Ala
306 305

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VERIFICATION SUMMARY

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L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:37 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:1
L:60 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:2
L:76 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:3
L:93 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:4
L:99 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:4
L:116 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:5
L:122 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:5
L:141 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:6
L:160 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:7
L:176 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:8